

GRADUATE LISTING

11.07 Opiate Receptors

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group.

0150: US 60/270,479
0151: 2001-02-22

Figure 1

170: FastSEQ for Windows Version 4.0

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0210: 1
0211: 81
0212: DNA
0213: Homo Sapiens

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90687
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(211) 26
(212) PRT
(213) Homo Sapiens

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:220:
:223: Peptide fragment

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400 2
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 His Lys Pro Val Leu Leu Trp Phe Cys Asp
 20 25

<210> 3
<211> 262
<212> DNA
<213> Homo sapiens

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971).
 2. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971).
 3. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971).
 4. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971).

<400> 3

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gaaatattat	caagagaaat	tacatata	gaaaaaaan	nnnnnnnnnn	aaaaaaan	180
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<400> 4NA

<400> Homo Sapiens

<400> 4

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cttcccaaga	tagtgatctc	catagattac	tataacatgt	tcaccagcat	attcacctc	180
tgaacatga	gtgttgatcg	atacatttgc	gtctgccacc	ctgtcaaggc	cttagatttc	240
agtaattctc	gaaatgcaa	aattatcaat	gtctgcaact	ggatcccttc	tcagatatt	300
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<400> 514

<400> 5PRT

<400> Homo Sapiens

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Lys	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile
		35				40					45				
Asp	Lys	Lys	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr	Met	Ser
	50			55					60						
Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe
65				70					75					80	
Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys	Asn	Trp	Ile	Leu
			85					90					95		
Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr	Lys	Tyr
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Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro	Thr	Trp
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Tyr	Trp	Arg	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala	Phe	Ile
	130					135				140					
Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile	Leu	Arg
145				150				155				160			
Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp	Arg	Asn

171
 181 Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val Phe Ile
 185 188 190
 Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val
 195 200 205
 Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile
 210 215 220
 Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe
 225 230 235 240
 Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr
 245 250 255
 Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr
 260 265 270
 Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln
 275 280 285
 Asn Tyr Tyr Ile Ile His Arg Leu Cys Cys Asn Thr Pro Leu Ile Ser
 290 295 300
 Gln Lys Pro Val Leu Leu Trp Phe Cys Asp
 305 310

111-141
 113-141
 113-141
 113-141

<400> 6

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<211> 476

<212> 121

113-141

<213> 7

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 35 40 45
 Leu Ala Thr Ser His Ser Gly Ala Arg Pro Ala Val Ser Thr Met Asp
 50 55 60
 Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala Leu Ala
 65 70 75 80
 Lys Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val Asn Leu
 85 90 95
 Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn Arg Thr
 100 105 110
 Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser Pro Ser
 115 120 125
 Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val
 130 135 140
 Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
 145 150 155 160
 Thr Lys Ser Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
 165 170 175
 Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
 180 185 190
 Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
 195 200 205
 Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
 210 215 220
 Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
 225 230 235 240
 Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Asn Val Cys Asn Trp
 245 250 255
 Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
 260 265 270
 Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
 275 280 285
 Thr Trp Tyr Trp Gln Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
 290 295 300
 Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
 305 310 315 320
 Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
 325 330 335
 Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
 340 345 350
 Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
 355 360 365
 Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
 370 375 380
 Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
 385 390 395 400
 Ala Phe Leu Asp Gln Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
 405 410 415
 Ser Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile Arg Gln
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<213> Homo Sapiens
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agtaacctga	400
ctttccagga	440
tgcacacatg	480
gtatctcccc	500
ctctctctctg	560
ctaaactctt	600
ctagcagctt	640
ctaaagactt	680
ctagcagctt	720
ctagcagctt	760
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ctagcagctt	1140
ctagcagctt	1160
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ctagcagctt	1200
ctagcagctt	1220
ctagcagctt	1240

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210: 9
211: 414
212: BRT
213: Homo Sapiens

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			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asp	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Ile	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
65					70					75				80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
			85						90					95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
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Asn	Tyr	Leu	Met	Ile	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
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 165 170 175
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 180 185 190
 Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
 195 200 205
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 210 215 220
 His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile
 225 230 235 240
 Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
 245 250 255
 Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Gln
 260 265 270
 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val His Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
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 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
 355 360 365
 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
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 Thr Asn His Gln Asn Tyr Tyr Ile Ile His Arg Leu Cys Cys Asn Thr
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<212> DNA

<213> Rattus norvegicus

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			20					25					30		
Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn	Arg	Thr
		35					40					45			
Asp	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser	Pro	Ser
	50					55					60				
Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val	Cys	Val
65					70					75				80	
Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val	Arg	Tyr
			85					90						95	
Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu
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Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr
		115					120					125			
Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile
	130					135					140				
Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr
145					150					155					160
Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu
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Arg	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys	Asn	Trp
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Met	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp
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Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe
305					310					315					320
Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr
			325						330					335	
Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg							

Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
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 Ile Ser Gln Lys Pro Val Leu Leu Trp Phe Cys Asp
 405 410

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 <212> DNA
 <213> Homo sapiens

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 gaaaggaagc ggcagaggcg cttggaaccc gaaaagtctc ggtgctctcg gctacctcgc 180
 acagcgggtgc cggcccgggc gtcagtacca tggacagcag cgtcgccccc acgaacgcga 240
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 taatgggaac atggccattt ggaaccatcc ttggcaagat agtgatctcc atagattact 660
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 totgcacccc tgtcaaggcc ttgattttcc gtactccccc aaatgpcaaa attatcaatg 780
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[111] 14
[111] 25
[111] DNA
[111] Homo Sapiens

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0010 Primer

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0001 15
0002 28
0003 DNA
0004 Homo Sapiens

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0213. Primer

0117 - FRT
0118 - FRT
0119 - FRT
0120 - Homo Sapiens

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[illegible]

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<210> 21
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 aaaaattata aggttttttg ctaaaactagg agttttaatcc attatagagg atgagaatgg 420
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 ttttttaata gaaatcatga aaaaaaannn aaaaaaanaa aaaaaaanaa atgtcggcgg 840
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<400> 22
 <400> 225
 <400> 228 DNA
 <400> 230 Homo Sapiens

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<400> 23
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 <400> 228 DNA
 <400> 230 Homo Sapiens

<400>
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 <400> n = A,T,C or G

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ctgtctgtaa gattttaatt taagcatata tttatgacct caacaaagac gaaccatctt 1600
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<210> 14

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<212> DNA

<213> Homo Sapiens

<220>

<223> Primer

<400> 14

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15

<210> 15

<211> 13

<212> DNA

<213> Homo Sapiens

<220>

<223> Primer

<400> 15

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23

<210> 16

<211> 19

<212> DNA

<213> Homo Sapiens

<220>

<223> Primer

<400> 16

ataattcata gatgttgctg caataccctt cttattttct

39

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial

[illegible]

29

- *211. "A"
- *212. "E"
- *213. DNA
- *213. Artificial Sequence

<220>
<223> Artificial

<400> 28
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20